



SEQUENCE LISTING

<110> DAI, KEN-SHOW

<120> HUMAN SCII-RELATED GENE VARIANTS ASSOCIATED WITH CANCERS

<130> U 014799-1

<140> 10/653,685

<141> 2003-09-02

<160> 6

<170> PatentIn version 3.2

<210> 1

<211> 1997

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (63)..(1574)

<400> 1

cggggaggaa tatgctgtgg agctcctctg ccatataaac aaaaagagga aatctttcaa 60

ac atg gct gaa gca aag acc cac tgg ctt gga gca gcc ctg tct ctt 107
Met Ala Glu Ala Lys Thr His Trp Leu Gly Ala Ala Leu Ser Leu
1 5 10 15

atc cct tta att ttc ctc atc tct ggg gct gaa gca gct tca ttt cag 155
Ile Pro Leu Ile Phe Leu Ile Ser Gly Ala Glu Ala Ala Ser Phe Gln
20 25 30

aga aac cag ctg ctt cag aaa gaa cca gac ctc agg ttg gaa aat gtc 203
Arg Asn Gln Leu Leu Gln Lys Glu Pro Asp Leu Arg Leu Glu Asn Val
35 40 45

caa aag ttt ccc agt cct gaa atg atc agg gct ttg gag tac ata gaa 251
Gln Lys Phe Pro Ser Pro Glu Met Ile Arg Ala Leu Glu Tyr Ile Glu
50 55 60

aac ccc ttt aaa cgc aca aat gaa ata gtg gag gaa caa tat act cct 299
Asn Pro Phe Lys Arg Thr Asn Glu Ile Val Glu Glu Gln Tyr Thr Pro
65 70 75

caa agc ctt gct aca ttg gaa tct gtc ttc caa gag ctg ggg aaa ctg 347
Gln Ser Leu Ala Thr Leu Glu Ser Val Phe Gln Glu Leu Gly Lys Leu
80 85 90 95

aca gga cca aac aac cag aaa cgt gag agg atg gat gag gag caa aaa 395
Thr Gly Pro Asn Asn Gln Lys Arg Glu Arg Met Asp Glu Glu Gln Lys
100 105 110

ctt tat acg gat gat gaa gat gat atc tac aag gct aat aac att gcc 443
Leu Tyr Thr Asp Asp Glu Asp Asp Ile Tyr Lys Ala Asn Asn Ile Ala
115 120 125

tat gaa gat gtg gtc ggg gga gaa gac tgg aac cca gta gag gag aaa 491

Tyr	Glu	Asp	Val	Val	Gly	Gly	Glu	Asp	Trp	Asn	Pro	Val	Glu	Glu	Lys	
		130					135					140				
ata	gag	agt	caa	acc	cag	gaa	gag	gtg	aga	gac	agc	aaa	gag	aat	ata	539
Ile	Glu	Ser	Gln	Thr	Gln	Glu	Glu	Val	Arg	Asp	Ser	Lys	Glu	Asn	Ile	
	145					150					155					
gga	aaa	aat	gaa	caa	atc	aac	gat	gag	atg	aaa	cgc	tca	ggg	cag	ctt	587
Gly	Lys	Asn	Glu	Gln	Ile	Asn	Asp	Glu	Met	Lys	Arg	Ser	Gly	Gln	Leu	
160					165					170					175	
ggc	atc	cag	gaa	gaa	gat	ctt	cgg	aaa	gag	agt	aaa	gac	caa	ctc	tca	635
Gly	Ile	Gln	Glu	Glu	Asp	Leu	Arg	Lys	Glu	Ser	Lys	Asp	Gln	Leu	Ser	
				180					185					190		
gat	gat	gtc	tcc	aaa	gta	att	gcc	tat	ttg	aaa	agg	tta	gta	aat	gct	683
Asp	Asp	Val	Ser	Lys	Val	Ile	Ala	Tyr	Leu	Lys	Arg	Leu	Val	Asn	Ala	
			195					200					205			
gca	gga	agt	ggg	agg	tta	cag	aat	ggg	caa	aat	ggg	gaa	agg	gcc	acc	731
Ala	Gly	Ser	Gly	Arg	Leu	Gln	Asn	Gly	Gln	Asn	Gly	Glu	Arg	Ala	Thr	
		210					215					220				
agg	ctt	ttt	gag	aaa	cct	ctt	gat	tct	cag	tct	att	tat	cag	ctg	att	779
Arg	Leu	Phe	Glu	Lys	Pro	Leu	Asp	Ser	Gln	Ser	Ile	Tyr	Gln	Leu	Ile	
	225					230					235					
gaa	atc	tca	agg	aat	tta	cag	ata	ccc	cca	gaa	gac	tta	att	gag	atg	827
Glu	Ile	Ser	Arg	Asn	Leu	Gln	Ile	Pro	Pro	Glu	Asp	Leu	Ile	Glu	Met	
240					245					250					255	
ctc	aaa	act	ggg	gag	aag	ccg	aat	gga	tca	gtg	gaa	ccg	gag	cgg	gag	875
Leu	Lys	Thr	Gly	Glu	Lys	Pro	Asn	Gly	Ser	Val	Glu	Pro	Glu	Arg	Glu	
				260					265					270		
ctt	gac	ctt	cct	gtt	gac	cta	gat	gac	atc	tca	gag	gct	gac	tta	gac	923
Leu	Asp	Leu	Pro	Val	Asp	Leu	Asp	Asp	Ile	Ser	Glu	Ala	Asp	Leu	Asp	
			275					280					285			
cat	cca	gac	ctg	ttc	caa	aat	agg	atg	ctc	tcc	aag	agt	ggc	tac	cct	971
His	Pro	Asp	Leu	Phe	Gln	Asn	Arg	Met	Leu	Ser	Lys	Ser	Gly	Tyr	Pro	
		290					295					300				
aaa	aca	cct	ggc	cgt	gct	ggg	act	gag	gcc	cta	cca	gac	ggg	ctc	agt	1019
Lys	Thr	Pro	Gly	Arg	Ala	Gly	Thr	Glu	Ala	Leu	Pro	Asp	Gly	Leu	Ser	
	305					310					315					
gtt	gag	gat	att	tta	aat	ctt	tta	ggg	atg	gag	agt	gca	gca	aat	cag	1067
Val	Glu	Asp	Ile	Leu	Asn	Leu	Leu	Gly	Met	Glu	Ser	Ala	Ala	Asn	Gln	
320					325					330					335	
aaa	acg	tcg	tat	ttt	ccc	aat	cca	tat	aac	cag	gag	aaa	gtt	ctg	cca	1115
Lys	Thr	Ser	Tyr	Phe	Pro	Asn	Pro	Tyr	Asn	Gln	Glu	Lys	Val	Leu	Pro	
				340					345					350		
agg	ctc	cct	tat	ggc	gct	gga	aga	tct	aga	tcg	aac	cag	ctt	ccc	aaa	1163
Arg	Leu	Pro	Tyr	Gly	Ala	Gly	Arg	Ser	Arg	Ser	Asn	Gln	Leu	Pro	Lys	
			355					360					365			
gct	gcc	tgg	att	cca	cat	gtt	gaa	aac	aga	cag	atg	gca	tat	gaa	aac	1211
Ala	Ala	Trp	Ile	Pro	His	Val	Glu	Asn	Arg	Gln	Met	Ala	Tyr	Glu	Asn	

370	375	380	
ctg aac gac aag gat caa gaa tta ggt gag tac ttg gcc agg atg cta			1259
Leu Asn Asp Lys Asp Gln Glu Leu Gly Glu Tyr Leu Ala Arg Met Leu			
385	390	395	
ggt aaa tac cct gag atc att aat tca aac caa gtg aag cga gtt cct			1307
Val Lys Tyr Pro Glu Ile Ile Asn Ser Asn Gln Val Lys Arg Val Pro			
400	405	410	415
ggt caa ggc tca tct gaa gat gac ctg cag gaa gag gaa caa att gag			1355
Gly Gln Gly Ser Ser Glu Asp Asp Leu Gln Glu Glu Glu Gln Ile Glu			
	420	425	430
cag gcc atc aaa gag cat ttg aat caa ggc agc tct cag gag act gac			1403
Gln Ala Ile Lys Glu His Leu Asn Gln Gly Ser Ser Gln Glu Thr Asp			
	435	440	445
aag ctg gcc ccg gtg agc aaa agg ttc cct gtg ggg ccc ccg aag aat			1451
Lys Leu Ala Pro Val Ser Lys Arg Phe Pro Val Gly Pro Pro Lys Asn			
	450	455	460
gat gat acc cca aat agg cag tac tgg gat gaa gat ctg tta atg aaa			1499
Asp Asp Thr Pro Asn Arg Gln Tyr Trp Asp Glu Asp Leu Leu Met Lys			
	465	470	475
gtg ctg gaa tac ctc aat caa gaa aag gca gaa aag gga agg gag cat			1547
Val Leu Glu Tyr Leu Asn Gln Glu Lys Ala Glu Lys Gly Arg Glu His			
480	485	490	495
att gct aag aga gca atg gaa aat atg taagctgctt tcattaatta			1594
Ile Ala Lys Arg Ala Met Glu Asn Met			
	500		
ccctactttc attcctccca ccccaagcaa atcccaacat ttctcttcag tgtgttgact			1654
tctatcctgt taacactgta atatctttaa atgatgtaca ggcagatgaa accagggtcac			1714
tggggagtct gcttcatttc ctctgagctg ttatcttgtg tatggatatg tgtaaatggt			1774
atgactcctt gataaaaaat ttattatgtc cattattcaa gaaagatatc tatgactgtg			1834
tttaatagta tatctaattg ctgtggcatt gttgatgctc acatatgata aaaaagtgtc			1894
ctataattct attgaaagtt tttaatatatt attgaattat tttgttactg tctgtagcgt			1954
tttgtggagt actggaccaa aaaaataaag cattataaat ata			1997

<210> 2
 <211> 504
 <212> PRT
 <213> Homo sapiens

<400> 2

Met	Ala	Glu	Ala	Lys	Thr	His	Trp	Leu	Gly	Ala	Ala	Leu	Ser	Leu	Ile
1				5					10					15	

Pro Leu Ile Phe Leu Ile Ser Gly Ala Glu Ala Ala Ser Phe Gln Arg

20										25					30															
Asn	Gln	Leu	Leu	Gln	Lys	Glu	Pro	Asp	Leu	Arg	Leu	Glu	Asn	Val	Gln															
		35					40					45																		
Lys	Phe	Pro	Ser	Pro	Glu	Met	Ile	Arg	Ala	Leu	Glu	Tyr	Ile	Glu	Asn															
	50					55					60																			
Pro	Phe	Lys	Arg	Thr	Asn	Glu	Ile	Val	Glu	Glu	Gln	Tyr	Thr	Pro	Gln															
65					70					75					80															
Ser	Leu	Ala	Thr	Leu	Glu	Ser	Val	Phe	Gln	Glu	Leu	Gly	Lys	Leu	Thr															
				85					90					95																
Gly	Pro	Asn	Asn	Gln	Lys	Arg	Glu	Arg	Met	Asp	Glu	Glu	Gln	Lys	Leu															
			100					105					110																	
Tyr	Thr	Asp	Asp	Glu	Asp	Asp	Ile	Tyr	Lys	Ala	Asn	Asn	Ile	Ala	Tyr															
		115					120					125																		
Glu	Asp	Val	Val	Gly	Gly	Glu	Asp	Trp	Asn	Pro	Val	Glu	Glu	Lys	Ile															
	130					135					140																			
Glu	Ser	Gln	Thr	Gln	Glu	Glu	Val	Arg	Asp	Ser	Lys	Glu	Asn	Ile	Gly															
145					150					155					160															
Lys	Asn	Glu	Gln	Ile	Asn	Asp	Glu	Met	Lys	Arg	Ser	Gly	Gln	Leu	Gly															
				165				170						175																
Ile	Gln	Glu	Glu	Asp	Leu	Arg	Lys	Glu	Ser	Lys	Asp	Gln	Leu	Ser	Asp															
			180					185					190																	
Asp	Val	Ser	Lys	Val	Ile	Ala	Tyr	Leu	Lys	Arg	Leu	Val	Asn	Ala	Ala															
		195					200					205																		
Gly	Ser	Gly	Arg	Leu	Gln	Asn	Gly	Gln	Asn	Gly	Glu	Arg	Ala	Thr	Arg															
		210				215					220																			
Leu	Phe	Glu	Lys	Pro	Leu	Asp	Ser	Gln	Ser	Ile	Tyr	Gln	Leu	Ile	Glu															
225					230					235					240															
Ile	Ser	Arg	Asn	Leu	Gln	Ile	Pro	Pro	Glu	Asp	Leu	Ile	Glu	Met	Leu															
				245					250					255																
Lys	Thr	Gly	Glu	Lys	Pro	Asn	Gly	Ser	Val	Glu	Pro	Glu	Arg	Glu	Leu															
			260					265					270																	

Asp Leu Pro Val Asp Leu Asp Asp Ile Ser Glu Ala Asp Leu Asp His
 275 280 285

Pro Asp Leu Phe Gln Asn Arg Met Leu Ser Lys Ser Gly Tyr Pro Lys
 290 295 300

Thr Pro Gly Arg Ala Gly Thr Glu Ala Leu Pro Asp Gly Leu Ser Val
 305 310 315 320

Glu Asp Ile Leu Asn Leu Leu Gly Met Glu Ser Ala Ala Asn Gln Lys
 325 330 335

Thr Ser Tyr Phe Pro Asn Pro Tyr Asn Gln Glu Lys Val Leu Pro Arg
 340 345 350

Leu Pro Tyr Gly Ala Gly Arg Ser Arg Ser Asn Gln Leu Pro Lys Ala
 355 360 365

Ala Trp Ile Pro His Val Glu Asn Arg Gln Met Ala Tyr Glu Asn Leu
 370 375 380

Asn Asp Lys Asp Gln Glu Leu Gly Glu Tyr Leu Ala Arg Met Leu Val
 385 390 395 400

Lys Tyr Pro Glu Ile Ile Asn Ser Asn Gln Val Lys Arg Val Pro Gly
 405 410 415

Gln Gly Ser Ser Glu Asp Asp Leu Gln Glu Glu Glu Gln Ile Glu Gln
 420 425 430

Ala Ile Lys Glu His Leu Asn Gln Gly Ser Ser Gln Glu Thr Asp Lys
 435 440 445

Leu Ala Pro Val Ser Lys Arg Phe Pro Val Gly Pro Pro Lys Asn Asp
 450 455 460

Asp Thr Pro Asn Arg Gln Tyr Trp Asp Glu Asp Leu Leu Met Lys Val
 465 470 475 480

Leu Glu Tyr Leu Asn Gln Glu Lys Ala Glu Lys Gly Arg Glu His Ile
 485 490 495

Ala Lys Arg Ala Met Glu Asn Met
 500

<210> 3
 <211> 2077
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (63)..(356)

```

<400> 3
cggggaggaa tatgctgtgg agctcctctg ccatataaac aaaaagagga aatctttcaa      60

ac atg gct gaa gca aag acc cac tgg ctt gga gca gcc ctg tct ctt      107
  Met Ala Glu Ala Lys Thr His Trp Leu Gly Ala Ala Leu Ser Leu
    1             5             10             15

atc cct tta att ttc ctc atc tct ggg gct gaa gca gct tca ttt cag      155
Ile Pro Leu Ile Phe Leu Ile Ser Gly Ala Glu Ala Ala Ser Phe Gln
          20             25             30

aga aac cag ctg ctt cag aaa gaa cca gac ctc agg ttg gaa aat gtc      203
Arg Asn Gln Leu Leu Gln Lys Glu Pro Asp Leu Arg Leu Glu Asn Val
          35             40             45

caa aag ttt ccc agt cct gaa atg atc agg gct ttg gag tac ata gaa      251
Gln Lys Phe Pro Ser Pro Glu Met Ile Arg Ala Leu Glu Tyr Ile Glu
          50             55             60

aac ctc cga caa caa gct cat aag aaa gaa agc tta agc aca tgc aat      299
Asn Leu Arg Gln Gln Ala His Lys Lys Glu Ser Leu Ser Thr Cys Asn
          65             70             75

tcc ctc cta tgt atg aag aga att cca ggg ata acc cct tta aac gca      347
Ser Leu Leu Cys Met Lys Arg Ile Pro Gly Ile Thr Pro Leu Asn Ala
          80             85             90             95

caa atg aaa tagtggagga acaatatact cctcaaagcc ttgctacatt      396
Gln Met Lys

ggaatctgtc ttccaagagc tggggaaaact gacaggacca aacaaccaga aacgtgagag      456

gatggatgag gagcaaaaac tttatacgga tgatgaagat gatatctaca aggctaataa      516

cattgcctat gaagatgtgg tcgggggaga agactggaac ccagtagagg agaaaataga      576

gagtcaaacc caggaagagg tgagagacag caaagagaat ataggaaaaa atgaacaaat      636

caacgatgag atgaaacgct cagggcagct tggcatccag gaagaagatc ttcggaaaga      696

gagtaaagac caactctcag atgatgtctc caaagtaatt gcctatttga aaaggttagt      756

aaatgctgca ggaagtggga gggttacagaa tgggcaaaat ggggaaaggg ccaccaggct      816

ttttgagaaa cctcttgatt ctcaagtctat ttatcagctg attgaaatct caaggaattt      876

acagataccc ccagaagact taattgagat gctcaaaact ggggagaagc cgaatggatc      936

agtggaaccg gagcggggagc ttgaccttcc tgttgaccta gatgacatct cagaggctga      996

```

cttagaccat ccagacctgt tccaaaatag gatgctctcc aagagtggct accctaaaac 1056
 acctgggtcgt gctgggactg aggccctacc agacgggctc agtggtgagg atattttaaa 1116
 tcttttaggg atggagagtg cagcaaataca gaaaacgtcg tattttccca atccatataa 1176
 ccaggagaaa gttctgcaa ggctccctta tgggtgctgga agatctagat cgaaccagct 1236
 tcccaaagct gcctggattc cacatgttga aaacagacag atggcatatg aaaacctgaa 1296
 cgacaaggat caagaattag gtgagtactt ggccaggatg ctagttaaat accctgagat 1356
 cattaattca aaccaagtga agcgagttcc tggcaaggc tcatctgaag atgacctgca 1416
 ggaagaggaa caaattgagc aggccatcaa agagcatttg aatcaaggca gctctcagga 1476
 gactgacaag ctggccccgg tgagcaaaag gttccctgtg gggccccga agaattgatga 1536
 taccctaaat aggcagtact gggatgaaga tctgttaatg aaagtgtgg aataacctca 1596
 tcaagaaaag gcagaaaagg gaaggagca tattgctaag agagcaatgg aaaatatgta 1656
 agctgctttc attaattacc ctactttcat tcctcccacc ccaagcaaat cccaacattt 1716
 ctcttcagtg tgttgacttc tctctgtta acactgtaat atctttaaat gatgtacagg 1776
 cagatgaaac caggtcactg gggagtctgc ttcatttcct ctgagctgtt atcttgtgta 1836
 tggatatgtg taaatgttat gactccttga taaaaaattt attatgtcca ttattcaaga 1896
 aagatatcta tgactgtgtt taatagtata tctaattggct gtggcattgt tgatgtcac 1956
 atatgataaa aaagtgtcct ataattctat tgaaagtttt taatatttat tgaattattt 2016
 tgttactgtc tgtagcgttt tgtggagtagc tggacccaaa aaataaagca ttataaatat 2076
 a 2077

<210> 4
 <211> 98
 <212> PRT
 <213> Homo sapiens

<220>
 <223> UNKNOWN

<400> 4

Met Ala Glu Ala Lys Thr His Trp Leu Gly Ala Ala Leu Ser Leu Ile
 1 5 10 15

Pro Leu Ile Phe Leu Ile Ser Gly Ala Glu Ala Ala Ser Phe Gln Arg
 20 25 30

Asn Gln Leu Leu Gln Lys Glu Pro Asp Leu Arg Leu Glu Asn Val Gln
 35 40 45

Lys Phe Pro Ser Pro Glu Met Ile Arg Ala Leu Glu Tyr Ile Glu Asn
 50 55 60

Leu Arg Gln Gln Ala His Lys Lys Glu Ser Leu Ser Thr Cys Asn Ser
 65 70 75 80

Leu Leu Cys Met Lys Arg Ile Pro Gly Ile Thr Pro Leu Asn Ala Gln
 85 90 95

Met Lys

<210> 5
 <211> 1803
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (63)..(539)

<400> 5
 cggggaggaa tatgctgtgg agctcctctg ccatataaac aaaaagagga aatctttcaa 60
 ac atg gct gaa gca aag acc cac tgg ctt gga gca gcc ctg tct ctt 107
 Met Ala Glu Ala Lys Thr His Trp Leu Gly Ala Ala Leu Ser Leu
 1 5 10 15
 atc cct tta att ttc ctc atc tct ggg gct gaa gca gct tca ttt cag 155
 Ile Pro Leu Ile Phe Leu Ile Ser Gly Ala Glu Ala Ala Ser Phe Gln
 20 25 30
 aga aac cag ctg ctt cag aaa gaa cca gac ctc agg ttg gaa aat gtc 203
 Arg Asn Gln Leu Leu Gln Lys Glu Pro Asp Leu Arg Leu Glu Asn Val
 35 40 45
 caa aag ttt ccc agt cct gaa atg atc agg gct ttg gag tac ata gaa 251
 Gln Lys Phe Pro Ser Pro Glu Met Ile Arg Ala Leu Glu Tyr Ile Glu
 50 55 60
 aac ctc cga caa caa gct cat aag gaa gaa agc agc cca gat tat aat 299
 Asn Leu Arg Gln Gln Ala His Lys Glu Glu Ser Ser Pro Asp Tyr Asn
 65 70 75
 ccc tac caa ggt gtc tct gtc ccc ctt cag caa aaa gaa aat ggc gat 347
 Pro Tyr Gln Gly Val Ser Val Pro Leu Gln Gln Lys Glu Asn Gly Asp
 80 85 90 95
 gaa agc cac ttg ccc gag agg gat tca ctg agt gaa gaa gac tgg atg 395
 Glu Ser His Leu Pro Glu Arg Asp Ser Leu Ser Glu Glu Asp Trp Met
 100 105 110
 aga ata ata ctc gaa gct ttg aga cag gct gaa aat gag cct cag tct 443
 Arg Ile Ile Leu Glu Ala Leu Arg Gln Ala Glu Asn Glu Pro Gln Ser
 115 120 125

gca cca aaa gaa aat aag ccc tat gcc ttg aat tca gaa aag aac ttt	491
Ala Pro Lys Glu Asn Lys Pro Tyr Ala Leu Asn Ser Glu Lys Asn Phe	
130 135 140	
cca atg gac atg agt gat gat tat gag aca cag cag tgg cca gaa aga	539
Pro Met Asp Met Ser Asp Asp Tyr Glu Thr Gln Gln Trp Pro Glu Arg	
145 150 155	
aagcttaagc acatgcaatt cctccttatg tatgaagaga attccaggga taaccctttt	599
aaacgcacaa atgaaatagt ggaggaacaa tatactcctc aaagccttgc tacattggaa	659
tctgtcttcc aagagctggg gaaactgaca ggaccaaaca accagaaacg tgagaggatg	719
gatgaggagc aaaaacttta tacggatgat gaagatgata tctacaaggc taataacatt	779
gcctatgaag atgtggtcgg gggagaagac tggaaccag tagaggagaa aatagagagt	839
caaaccagc aagaggtgag agacagcaaa gagaatatag gaaaaaatga acaaatcaac	899
gatgagatga aacgctcagg gcagcttggc atccaggaag aagatcttcg gaaagagagt	959
aaagaccaac ttcagatga tgtctccaaa gtaattgcct atttgaaaag gttagtaa	1019
gctgcaggaa gtgggaggtt acagaatggg caaaatgggg aaagggccac caggcttttt	1079
gagaaacctc ttgattctca gtctatttat cagctgattg aaatctcaag gaatttacag	1139
atacccccag aagacttaat tgagatgctc aaaactgggg agaagccgaa tggatcagt	1199
gaaccggagc gggagcttga ccttctgtt gacctagatg acatctcaga ggctgactta	1259
gaccatccag acctgttcca aaataggatg ctctccaaga gtggctacct taaaacacct	1319
ggctgtgctg ggactgaggc cctaccagac gggctcagtg ttgaggatat tttaa	1379
ttagggatg agagtgcagc aaatcagaaa acgtcgtatt ttcccaagca aatcccaaca	1439
tttctcttca gtgtgttgac ttctatcctg ttaacactgt aatatcttta aatgatgtac	1499
aggcagatga aaccagggtca ctggggagtc tgcttcattt cctctgagct gttatcttgt	1559
gtatggatat gtgtaaatgt tatgactcct tgataaaaaa tttattatgt ccattattca	1619
agaaagatat ctatgactgt gtttaaatagt atatcta	1679
cacatatgat aaaaaagtgt cctataattc tattgaaagt tttta	1739
ttttgttact gtctgtagcg ttttgtggag tactggacca aaaaaataaa gcattataaa	1799
tata	1803

<210> 6
 <211> 159
 <212> PRT
 <213> Homo sapiens

<220>
 <223> UNKNOWN

<400> 6

Met Ala Glu Ala Lys Thr His Trp Leu Gly Ala Ala Leu Ser Leu Ile
1 5 10 15

Pro Leu Ile Phe Leu Ile Ser Gly Ala Glu Ala Ala Ser Phe Gln Arg
20 25 30

Asn Gln Leu Leu Gln Lys Glu Pro Asp Leu Arg Leu Glu Asn Val Gln
35 40 45

Lys Phe Pro Ser Pro Glu Met Ile Arg Ala Leu Glu Tyr Ile Glu Asn
50 55 60

Leu Arg Gln Gln Ala His Lys Glu Glu Ser Ser Pro Asp Tyr Asn Pro
65 70 75 80

Tyr Gln Gly Val Ser Val Pro Leu Gln Gln Lys Glu Asn Gly Asp Glu
85 90 95

Ser His Leu Pro Glu Arg Asp Ser Leu Ser Glu Glu Asp Trp Met Arg
100 105 110

Ile Ile Leu Glu Ala Leu Arg Gln Ala Glu Asn Glu Pro Gln Ser Ala
115 120 125

Pro Lys Glu Asn Lys Pro Tyr Ala Leu Asn Ser Glu Lys Asn Phe Pro
130 135 140

Met Asp Met Ser Asp Asp Tyr Glu Thr Gln Gln Trp Pro Glu Arg
145 150 155